WHAT IS CLAIMED IS:

1. A hybridization assay probe for detecting a nucleic acid, comprising:

a probe sequence that comprises

a target-complementary sequence of bases, and optionally

one or more base sequences that are not complementary to said nucleic acid that is to be detected,

wherein said target-complementary sequence of bases consists of 12-87 contiguous bases contained within the sequence of SEQ ID NO:101 or the complement thereof, allowing for the presence of RNA and DNA equivalents, nucleotide analogs and up to 10% base differences, and

wherein said hybridization assay probe has a length of up to 100 bases.

2. The hybridization assay probe of Claim 1, wherein said target-complementary sequence of bases consists of 12-69 contiguous bases contained within the sequence of SEQ ID NO:102 or the complement thereof, allowing for the presence of RNA and DNA equivalents, nucleotide analogs and up to 10% base differences.

3. The hybridization assay probe of Claim 2, wherein said hybridization assay probe comprises said optional one or more base sequences that are not complementary to said nucleic acid that is to be detected.

4. The hybridization assay probe of Claim 3, further comprising a detectable label.

5. The hybridization assay probe of Claim 3, further comprising a fluorophore moiety and a quencher moiety, said hybridization assay probe being a molecular beacon.

6. The hybridization assay probe of Claim 5, wherein said target-complementary sequence of bases consists of any one of either SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182 or SEQ ID NO:183.

7. The hybridization assay probe of Claim 2, wherein said probe sequence does not comprise said optional one or more base sequences that are not complementary to said nucleic acid that is to be detected.

8. The hybridization assay probe of Claim 7, wherein said hybridization assay probe has a length of up to 69 bases.

9. The hybridization assay probe of Claim 8, further comprising a detectable label.

10. The hybridization assay probe of Claim 2, wherein said target-complementary sequence of bases consists of 18-52 contiguous bases contained within the sequence of SEQ ID NO:103 or the complement thereof, allowing for the presence of RNA and DNA equivalents, nucleotide analogs and up to 10% base differences.

11. The hybridization assay probe of Claim 10, wherein said probe sequence does not comprise said optional one or more base sequences that are not complementary to said nucleic acid that is to be detected.

12. The hybridization assay probe of Claim 11, further comprising a detectable label.

13. The hybridization assay probe of Claim 12, wherein said detectable label is selected from the group consisting of a chemiluminescent label and a fluorescent label.

14. The hybridization assay probe of Claim 10, wherein said hybridization assay probe has a length of up to 52 bases.

15. The hybridization assay probe of Claim 14, wherein said target-complementary sequence of bases consists of 18-22 contiguous bases contained within the sequence of SEQ ID NO:103 or the complement thereof, allowing for the presence of RNA and DNA equivalents, nucleotide analogs and up to 10% base differences, and wherein said hybridization assay probe has a length of up to 22 bases.

16. The hybridization assay probe of Claim 1, wherein said probe sequence consists of SEQ ID NO:116.

17. The hybridization assay probe of Claim 15, wherein said probe sequence is selected from the group consisting of SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111 and SEQ ID NO:114.

18. A kit for amplifying a target nucleic acid sequence that may be present in a biological sample, comprising:

a first primer that comprises a 3' terminal target-complementary sequence and optionally a first primer upstream sequence that is not complementary to said target nucleic acid sequence that is to be amplified, said 3' terminal target-complementary sequence of said first primer comprising 22 contiguous bases contained within SEQ ID NO:73, allowing for the presence of RNA and DNA equivalents, nucleotide analogs and up to 10% base differences; and

a second primer that comprises a 3' terminal target-complementary sequence and

optionally a second primer upstream sequence that is not complementary to said target nucleic acid sequence that is to be amplified, said 3' terminal target-complementary sequence of said second primer comprising 18 contiguous bases contained within SEQ ID NO:59, allowing for the presence of RNA and DNA equivalents, nucleotide analogs and up to 10% base differences.

19. The kit of Claim 18, wherein said first primer and said second primer are each up to 60 bases in length.

20. The kit of Claim 18, wherein said 3' terminal target-complementary sequence of said first primer and said 3' terminal target-complementary sequence of said second primer are each up to 35 bases in length.

21. The kit of Claim 20, wherein said 3' terminal target-complementary sequence of said first primer is up to 24 bases in length.

22. The kit of Claim 20, wherein said 3' terminal target-complementary sequence of said second primer is up to 22 bases in length.

23. The kit of Claim 21, wherein said 3' terminal target-complementary sequence of said second primer is up to 22 bases in length.

24. The kit of Claim 23, wherein said first primer comprises said first primer upstream sequence.

25. The kit of Claim 24, wherein said first primer upstream sequence comprises a promoter sequence for T7 RNA polymerase.

26. The kit of Claim 23, wherein said 3' terminal target-complementary sequence of said first primer is selected from the group consisting of SEQ ID NO:75, SEQ ID NO:76 and SEQ ID NO:77, and wherein said 3' terminal target-complementary sequence of said second primer is selected from the group consisting of SEQ ID NO:60, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70 and SEQ ID NO:71.

27. The kit of Claim 21, wherein said 3' terminal target-complementary sequence of said first primer comprises 22 contiguous bases contained within SEQ ID NO:74, allowing for the presence of RNA and DNA equivalents, nucleotide analogs and up to 10% base differences.

28. The kit of Claim 27, wherein said 3' terminal target-complementary sequence of said second primer is up to 22 bases in length.

29. The kit of Claim 27, wherein said first primer comprises said first primer

upstream sequence.

30. The kit of Claim 29, wherein said first primer upstream sequence comprises a promoter sequence for T7 RNA polymerase.

31. A hybridization assay probe for detecting a nucleic acid, comprising:

a probe sequence that comprises

a target-complementary sequence of bases, and optionally

one or more base sequences that are not complementary to said nucleic acid that is to be detected,

wherein said target-complementary sequence of bases consists of 10-20 contiguous bases contained within the sequence of SEQ ID NO:99 or the complement thereof, allowing for the presence of RNA and DNA equivalents, nucleotide analogs and up to 10% base differences, and

wherein said hybridization assay probe has a length of up to 100 bases.

32. The hybridization assay probe of Claim 31, wherein said length of said hybridization assay probe is up to 30 bases.

33. The hybridization assay probe of Claim 32, wherein said probe sequence comprises said optional one or more base sequences that are not complementary to said nucleic acid that is to be detected.

34. The hybridization assay probe of Claim 33, further comprising a detectable label.

35. The hybridization assay probe of Claim 33, further comprising a fluorophore moiety and a quencher moiety, said hybridization assay probe being a molecular beacon.

36. The hybridization assay probe of Claim 31, wherein said probe sequence consists of 10-20 contiguous bases contained within the sequence of SEQ ID NO:99 or the complement thereof, allowing for the presence of RNA and DNA equivalents, nucleotide analogs and up to 10% base differences, and does not comprise said optional one or more base sequences that are not complementary to said WNV nucleic acids.

37. The hybridization assay probe of Claim 36, wherein said hybridization assay probe has a length of up to 20 bases.

38. The hybridization assay probe of Claim 32, wherein said target-complementary

sequence of bases consists of 19-20 contiguous bases contained within the sequence of SEQ ID NO:99 or the complement thereof, allowing for the presence of RNA and DNA equivalents, nucleotide analogs and up to 10% base differences.

39. The hybridization assay probe of Claim 38, wherein said probe sequence consists of 19-20 contiguous bases contained within the sequence of SEQ ID NO:99 or the complement thereof, allowing for the presence of RNA and DNA equivalents, nucleotide analogs and up to 10% base differences, and does not comprise said optional one or more base sequences that are not complementary to said nucleic acid that is to be detected.

40. The hybridization assay probe of Claim 38, further comprising a detectable label.

41. The hybridization assay probe of Claim 40, wherein said detecatble label is selected from the group consisting of a chemiluminescent label and a fluorescent label.

42. The hybridization assay probe of Claim 38, wherein said target-complementary sequence of bases consists of 19-20 contiguous bases contained within the sequence of SEQ ID NO:99 or the complement thereof, allowing for the presence of RNA and DNA equivalents, nucleotide analogs and up to 10% base differences, and wherein said hybridization assay probe has a length of up to 20 bases.

43. The hybridization assay probe of Claim 33, wherein said target-complementary sequence of bases acids is selected from the group consisting of SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169 and SEQ ID NO:170.

44. The hybridization assay probe of Claim 42, wherein said probe sequence is SEQ ID NO:100.

45. A kit for amplifying a target nucleic acid sequence that may be present in a biological sample, comprising:

a first primer that comprises a 3' terminal target-complementary sequence and optionally a first primer upstream sequence that is not complementary to said target nucleic acid sequence that is to be amplified, said 3' terminal target-complementary sequence of said first primer comprising 22 contiguous bases contained within SEQ ID NO:52, allowing for the presence of RNA and DNA equivalents, nucleotide analogs and up to 10% base differences; and

a second primer that comprises a 3' terminal target-complementary sequence and

optionally a second primer upstream sequence that is not complementary to said target nucleic acid sequence that is to be amplified, said 3' terminal target-complementary sequence of said second primer comprising 22 contiguous bases contained within SEQ ID NO:41, allowing for the presence of RNA and DNA equivalents, nucleotide analogs and up to 10% base differences.

46. The kit of Claim 45, wherein said first primer and said second primer are each up to 60 bases in length.

47. The kit of Claim 45, wherein said 3' terminal target-complementary sequence of said first primer and said 3' terminal target-complementary sequence of said second primer are each up to 35 bases in length.

48. The kit of Claim 47, wherein said 3' terminal target-complementary sequence of said first primer is up to 26 bases in length.

49. The kit of Claim 47, wherein said 3' terminal target-complementary sequence of said second primer is up to 23 bases in length.

50. The kit of Claim 48, wherein said 3' terminal target-complementary sequence of said second primer is up to 23 bases in length.

51. The kit of Claim 50, wherein said 3' terminal target-complementary sequence of said first primer is selected from the group consisting of SEQ ID NO:53, SEQ ID NO:54 and SEQ ID NO:55, and wherein said 3' terminal target-complementary sequence of said second primer is selected from the group consisting of SEQ ID NO:42, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:43, SEQ ID NO:49, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:50, SEQ ID NO:51 and SEQ ID NO:46.

52. The kit of Claim 48, wherein said 3' terminal target-complementary sequence of said second primer is up to 23 bases in length.

53. The kit of Claim 52, wherein said first primer comprises said first primer upstream sequence.

54. The kit of Claim 53, wherein said first primer upstream sequence comprises a promoter sequence for T7 RNA polymerase.

55. A hybridization assay probe for detecting a nucleic acid, comprising:

a probe sequence that comprises

a target-complementary sequence of bases, and optionally

one or more base sequences that are not complementary to said nucleic

acid that is to be detected,

wherein said target-complementary sequence of bases consists of 13-37 contiguous bases contained within the sequence of SEQ ID NO:95 or the complement thereof, allowing for the presence of RNA and DNA equivalents, nucleotide analogs and up to 10% base differences, and

wherein said hybridization assay probe has a length of up to 100 bases.

56. The hybridization assay probe of Claim 55, wherein said length of said hybridization assay probe is up to 37 bases.

57. The hybridization assay probe of Claim 56, wherein said hybridization assay probe comprises said optional one or more base sequences that are not complementary to said nucleic acid that is to be detected.

58. The hybridization assay probe of Claim 57, further comprising a detectable label.

59. The hybridization assay probe of Claim 57, further comprising a fluorophore moiety and a quencher moiety, said hybridization assay probe being a molecular beacon.

60. The hybridization assay probe of Claim 55, wherein said probe sequence consists of 13-20 contiguous bases contained within the sequence of SEQ ID NO:95 or the complement thereof, allowing for the presence of RNA and DNA equivalents, nucleotide analogs and up to 10% base differences, and does not comprise said optional one or more base sequences that are not complementary to said nucleic acid that is to be detected.

61. The hybridization assay probe of Claim 56, wherein said target-complementary sequence of bases consists of 13-20 contiguous bases contained within the sequence of SEQ ID NO:95 or the complement thereof, allowing for the presence of RNA and DNA equivalents, nucleotide analogs and up to 10% base differences.

62. The hybridization assay probe of Claim 61, wherein said probe sequence consists of 20 contiguous bases contained within the sequence of SEQ ID NO:95 or the complement thereof, allowing for the presence of RNA and DNA equivalents, nucleotide analogs and up to 10% base differences, and does not comprise said optional one or more base sequences that are not complementary to said nucleic acid that is to be detected.

63. The hybridization assay probe of Claim 61, further comprising a detectable label.

64. The hybridization assay probe of Claim 63, wherein said detecatble label is selected from the group consisting of a chemiluminescent label and a fluorescent label.

65. The hybridization assay probe of Claim 61, wherein said target-complementary sequence of bases consists of 13-20 contiguous bases contained within the sequence of SEQ ID NO:95 or the complement thereof, allowing for the presence of RNA and DNA equivalents, nucleotide analogs and up to 10% base differences, wherein said probe sequence does not comprise said optional one or more base sequences that are not complementary to said nucleic acid that is to be detected, and wherein said hybridization assay probe has a length of up to 20 bases.

66. The hybridization assay probe of Claim 57, wherein said target-complementary sequence of bases is selected from the group consisting of SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, and SEQ ID NO:158.

67. The hybridization assay probe of Claim 65, wherein said probe sequence is SEQ ID NO:98.

68. A kit for amplifying a target nucleic acid sequence that may be present in a biological sample, comprising:

a first primer that comprises a 3' terminal target-complementary sequence and optionally a first primer upstream sequence that is not complementary to said target nucleic acid sequence that is to be amplified, said 3' terminal target-complementary sequence of said first primer comprising 20 contiguous bases contained within SEQ ID NO:16, allowing for the presence of RNA and DNA equivalents, nucleotide analogs and up to 10% base differences; and

a second primer that comprises a 3' terminal target-complementary sequence up to 30 bases in length and optionally a second primer upstream sequence that is not complementary to said target nucleic acid sequence that is to be amplified, said 3' terminal target-complementary sequence of said second primer comprising 20 contiguous bases contained within SEQ ID NO:1, allowing for the presence of RNA and DNA equivalents, nucleotide analogs and up to 10% base differences.

69. The kit of Claim 68, wherein said first primer and said second primer are each up to 60 bases in length.

70. The kit of Claim 68, wherein said 3' terminal target-complementary sequence of said first primer is up to 35 bases in length.

71. The kit of Claim 70, wherein said 3' terminal target-complementary sequence of said first primer is up to 24 bases in length.

72. The kit of Claim 70, wherein said 3' terminal target-complementary sequence of said second primer is up to 24 bases in length.

73. The kit of Claim 71, wherein said 3' terminal target-complementary sequence of said second primer is up to 24 bases in length.

74. The kit of Claim 70, wherein said 3' terminal target-complementary sequence of said second primer is up to 26 bases in length and comprises 20 contiguous bases contained within SEQ ID NO:2, allowing for the presence of RNA and DNA equivalents, nucleotide analogs and up to 10% base differences.

75. The kit of Claim 74, wherein said 3' terminal target-complementary sequence of said first primer is up to 24 bases in length.

76. The kit of Claim 74, wherein said 3' terminal target-complementary sequence of said second primer is up to 24 bases in length.

77. The kit of Claim 75, wherein said 3' terminal target-complementary sequence of said second primer is up to 24 bases in length.

78. The kit of Claim 75, wherein said 3' terminal target-complementary sequence of said first primer is selected from the group consisting of SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26 and SEQ ID NO:28.

79. The kit of Claim 75, wherein said 3' terminal target-complementary sequence of said second primer is selected from the group consisting of SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:13 and SEQ ID NO:15.

80. The kit of Claim 78, wherein said 3' terminal target-complementary sequence of said second primer is selected from the group consisting of SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:13 and SEQ ID NO:15.

81. The kit of Claim 80, wherein said first primer comprises said first primer upstream sequence.

82. The kit of Claim 81, wherein said first primer upstream sequence comprises a promoter sequence for T7 RNA polymerase.